FIG. 1A

FIG. 1B

FIG. 1C

FIG. 2A

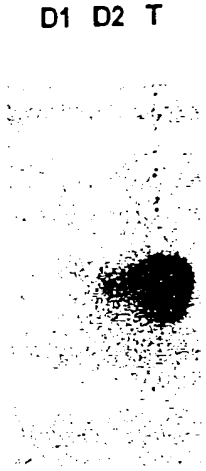


FIG. 2B

FIG. 2C

FIG. 2D

FIG. 3A

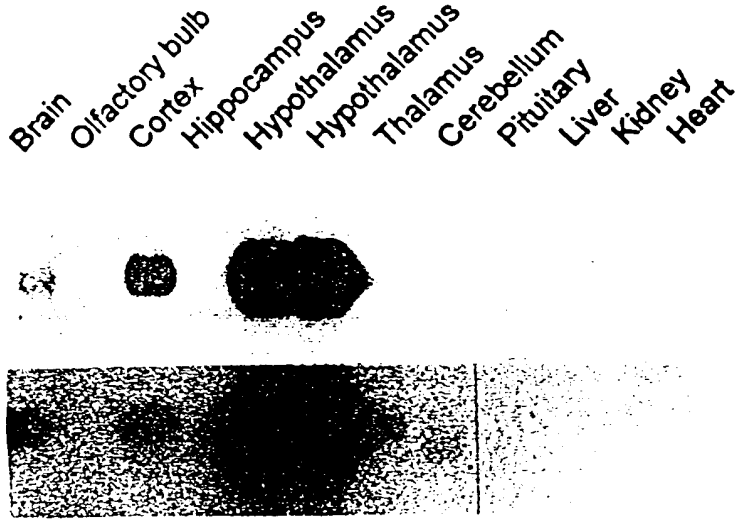


FIG. 3B

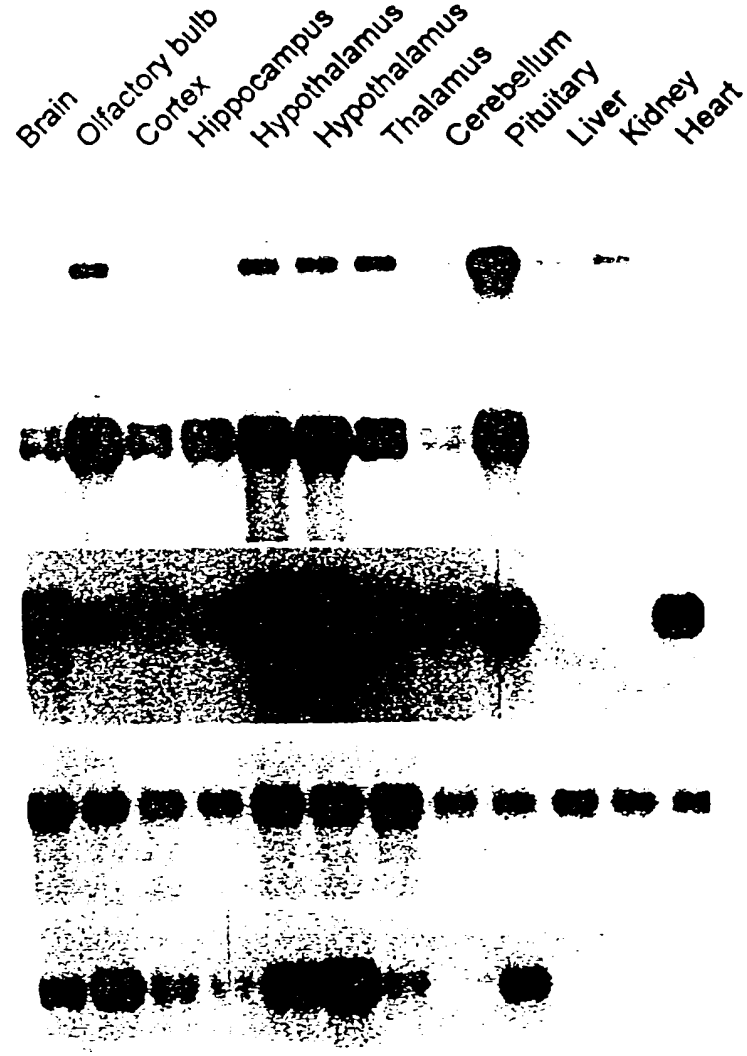


FIG. 3C

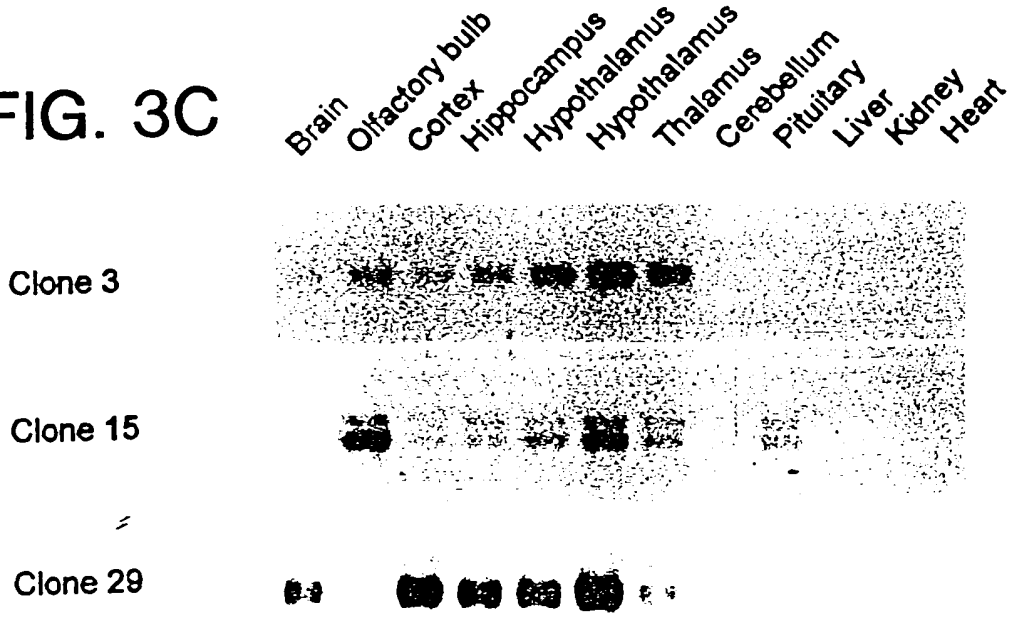
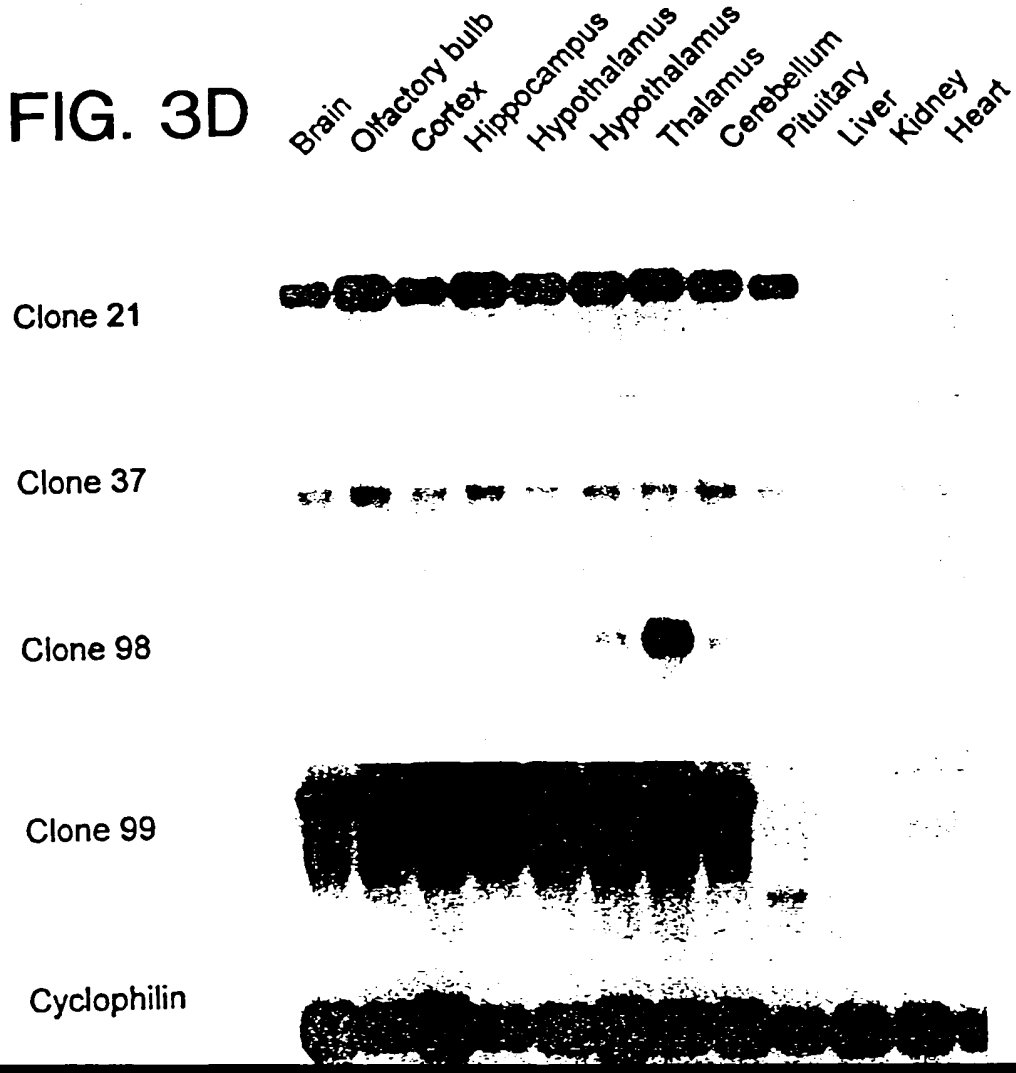


FIG. 3D



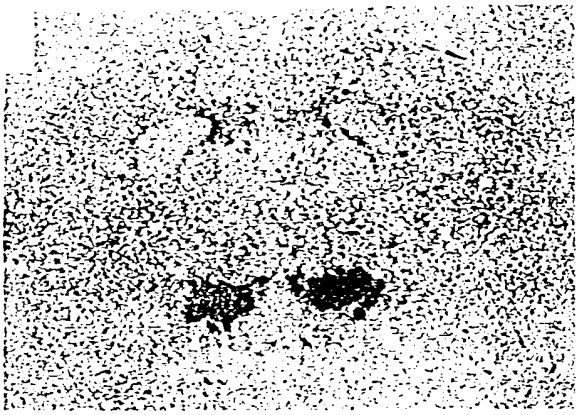


FIG. 4A

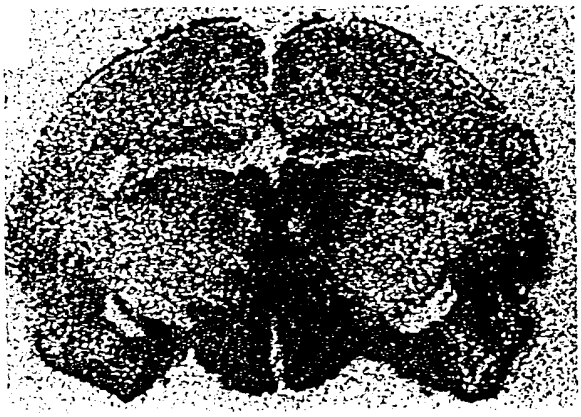


FIG. 4B

FIG. 4C

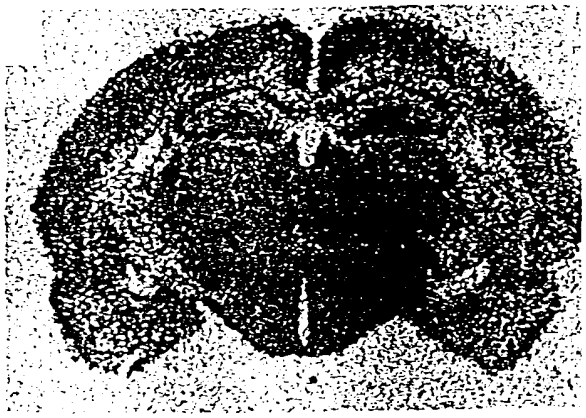


FIG. 4D

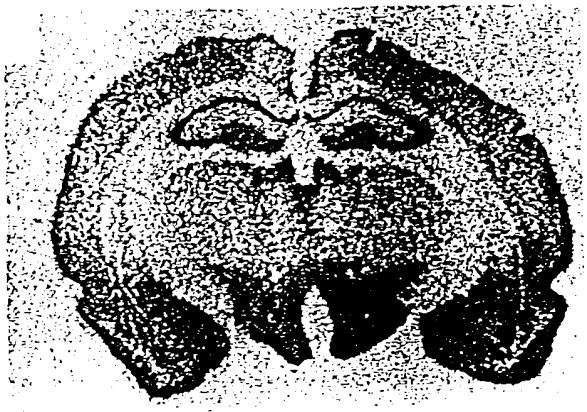


FIG. 4E

FIG. 4F

FIG. 5A

```
M   N   L/F P   S   T   K   V   P   W   A   A   V   T   L   L
ATG AAC CTT CCT TCT ACA AAG GTT CCC TGG GCC GCC GTG ACG CTG CTG
ATG AAC TTT CCT TCT ACA AAG GTT CCC TGG GCC GCC GTG ACG CTG CTG
        *

L   L   L   L   L   P   P   A   L   L   S   L   G   V   D   A
CTG CTG CTA CTG CTG CCG CCG GCG CTG CTG TCG CTT GGG GTG GAC GCG
CTG CTG CTA CTG CTG CCG CCG GCG CTG CTG TCG CTT GGG GTG GAC GCA
                                                        *

Q   P   L   P   D   C   C   R   Q   K   T   C   S   C   R   L
CAG CCT CTG CCC GAC TGC TGT CGC CAG AAG ACG TGT TCC TGC CGT CTC
CAG CCT CTG CCC GAC TGC TGT CGC CAG AAG ACG TGT TCC TGC CGT CTC

Y   E   L   L   H   G   A   G   N   H   A   A   G   I   L   T
TAC GAA CTG TTG CAC GGA GCT GGC AAC CAC GCC GCG GGC ATC CTC ACT
TAC GAA CTG TTG CAC GGA GCT GGC AAC CAC GCT GCG GGT ATC CTG ACT
                                        *       *       *

L   G   K   R   R   P   G   P   P   G   L   Q   G   R   L   Q
CTG GGA AAG CGG CGA CCT GGA CCC CCA GGC CTC CAA GGA CGG CTG CAG
CTG GGA AAG CGG CGG CCT GGA CCT CCA GGC CTC CAG GGA CGG CTG CAG
                    *           *           *

R   L   L   Q   A   N   G   N   H   A   A   G   I   L   T   M
CGC CTC CTT CAG GCC AAC GGT AAC CAC GCA GCT GGC ATC CTG ACC ATG
CGC CTC CTT CAG GCC AAC GGT AAC CAC GCA GCT GGC ATC CTG ACC ATG

G   R   R   A   G   A   E   L   E   P   Y/H P   C   P/S G   R
GGC CGC CGC GCA GGC GCA GAG CTA GAG CCA TAT CCC TGC CCT GGT CGC
GGC CGC CGC GCA GGC GCA GAG CTA GAG CCA CAT CCC TGC TCT GGT CGC
                                        *           *

R/G C   P   T   A/V T   A/T T   A   L   A   P   R   G   G   S
CGC TGT CCG ACT GCA ACC GCC ACC GCT TTA GCG CCC CGG GGC GGA TCC
GGC TGT CCG ACC GTA ACT ACC ACC GCT TTA GCA CCC CGG GGA GGG TCC
*               *   *     * *                   *               *   *

R/G V
AGA GTC TGA
GGA GTC TGA
*
```

FIG. 5B

```
consensus:                                    RL  LL   GNHAAGILT G
hcrt1:      LGVDAQPLPDCCRQKTCSCRLYELLHGAGNHAAGILTLG
hcrt2:                    PGPPGLQGRLQRLLQANGNHAAGILTMG
SECRETIN:     HSDGTFTSKLSRLRDSARLQRLLQGLV HSDGTFTSK
                                    * ********   ** ** *
```

```
                GCTAGGAGACATTGCGGCGGCGGTGGCGGCGTTGGCAGCAGCTGCAGACATGCTGCTGCT
1               ---------+---------+---------+---------+---------+---------+   60
                CGATCCTCTGTAACGCCGCCGCCACCGCCGCAACCGTCGTCGACGTCTGTACGACGACGA
                                                          M  L  L  L

                CAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCGGG
61              ---------+---------+---------+---------+---------+---------+  120
                GTTCTTTGTCTGCCTCCTGTAGTCGTCACAGATACTCTAGGCCCTCTTCGACCCGAGCCC
                 K  K  Q  T  E  D  I  S  S  V  Y  E  I  R  E  K  L  G  S  G

                TGCCTTCTCTGAGGTGATGCTGGCCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAA
121             ---------+---------+---------+---------+---------+---------+  180
                ACGGAAGAGACTCCACTACGACCGGGTCCTTTCCCCGAGACGAGTAGAACACCGGGAGTT
                 A  F  S  E  V  M  L  A  Q  E  R  G  S  A  H  L  V  A  L  K

                GTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCAGT
181             ---------+---------+---------+---------+---------+---------+  240
                CACGTAAGGGTTCTTTCGTGAAGCCCCGTTCCTCCGGGACCACCTCTTACTCTAGCGTCA
                 C  I  P  K  K  A  L  R  G  K  E  A  L  V  E  N  E  I  A  V

                ACTCCGCAGGATTAGCCACCCCAACATTGTGGCTCTGGAGGACGTCCACGAGAGCCCTTC
241             ---------+---------+---------+---------+---------+---------+  300
                TGAGGCGTCCTAATCGGTGGGGTTGTAACACCGAGACCTCCTGCAGGTGCTCTCGGGAAG
                 L  R  R  I  S  H  P  N  I  V  A  L  E  D  V  H  E  S  P  S

                CCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACTGTTTGACCGAATCATGGA
301             ---------+---------+---------+---------+---------+---------+  360
                GGTAGAGATGAACCGGTACCTCGACCATTGTCCACCACTTGACAAACTGGCTTAGTACCT
                 H  L  Y  L  A  M  E  L  V  T  G  G  E  L  F  D  R  I  M  E

                GCGGGGCTCCTACACAGAGAAGGATGCGAGCCACCTTGTAGGGCAGGTCCTTGGTGCTGT
361             ---------+---------+---------+---------+---------+---------+  420
                CGCCCCGAGGATGTGTCTCTTCCTACGCTCGGTGGAACATCCCGTCCAGGAACCACGACA
                 R  G  S  Y  T  E  K  D  A  S  H  L  V  G  Q  V  L  G  A  V

                CTCCTACCTTCATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAAAACCTCCTCTA
421             ---------+---------+---------+---------+---------+---------+  480
                GAGGATGGAAGTATCGGACCCGTAGCACGTGGCCCTGGAGTTCGGACTTTTGGAGGAGAT
                 S  Y  L  H  S  L  G  I  V  H  R  D  L  K  P  E  N  L  L  Y

                TGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATTCA
481             ---------+---------+---------+---------+---------+---------+  540
                ACGGTGTGGAAAACTCCTGAGGTTCTAGTACCAGAGACTGAAACCGGACAGGTTTTAAGT
                 A  T  P  F  E  D  S  K  I  M  V  S  D  F  G  L  S  K  I  Q
```

FIG. 6A

```
                AGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCAGGATATGTGGCCCCAGAGCTCCT
541             ---------+---------+---------+---------+---------+---------+  600
                TCGACCGTTGTACGATCCGTGTCGGACACCCTGGGGTCCTATACACCGGGGTCTCGAGGA
                 A  G  N  M  L  G  T  A  C  G  T  P  G  Y  V  A  P  E  L  L

                GGAGCAGAAACCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGTGTCATCTCCTACAT
601             ---------+---------+---------+---------+---------+---------+  660
                CCTCGTCTTTGGGATGCCCTTCCGGCATCTACACACCCGGGACCCACAGTAGAGGATGTA
                 E  Q  K  P  Y  G  K  A  V  D  V  W  A  L  G  V  I  S  Y  I

                CCTGCTGTGTGGGTACCCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGAT
661             ---------+---------+---------+---------+---------+---------+  720
                GGACGACACACCCATGGGGGGGGAAGATACTACTCTCGCTAGGACTTGAGAAGTCGGTCTA
                 L  L  C  G  Y  P  P  F  Y  D  E  S  D  P  E  L  F  S  Q  I

                TCTGAGGGCCAGCTACGAGTTTGACTCTCCCTTTTGGGATGACATCTCAGAATCAGCCAA
721             ---------+---------+---------+---------+---------+---------+  780
                AGACTCCCGGTCGATGCTCAAACTGAGAGGGAAAACCCTACTGTAGAGTCTTAGTCGGTT
                 L  R  A  S  Y  E  F  D  S  P  F  W  D  D  I  S  E  S  A  K

                AGACTTCATTCGGCACCTTCTGGAACGTGATCCCCAGAAGAGGTTCACCTGCCAACAGGC
781             ---------+---------+---------+---------+---------+---------+  840
                TCTGAAGTAAGCCGTGGAAGACCTTGCACTAGGGGTCTTCTCCAAGTGGACGGTTGTCCG
                 D  F  I  R  H  L  L  E  R  D  P  Q  K  R  F  T  C  Q  Q  A

                CTTACAGCATCTCTGGATCTCTGGGGATGCAGCCTTGGACAGGGACATCCTAGGTTCTGT
841             ---------+---------+---------+---------+---------+---------+  900
                GAATGTCGTAGAGACCTAGAGACCCCTACGTCGGAACCTGTCCCTGTAGGATCCAAGACA
                 L  Q  H  L  W  I  S  G  D  A  A  L  D  R  D  I  L  G  S  V

                CAGTGAGCAGATCCAGAAGAATTTTGCCAGGACCCACTGGAAGCGTGCATTCAATGCCAC
901             ---------+---------+---------+---------+---------+---------+  960
                GTCACTCGTCTAGGTCTTCTTAAAACGGTCCTGGGTGACCTTCGCACGTAAGTTACGGTG
                 S  E  Q  I  Q  K  N  F  A  R  T  H  W  K  R  A  F  N  A  T

                ATCATTCCTACGTCACATCCGTAAGCTGGGACAGAGCCCAGAGGGTGAGGAGGCCTCCAG
961             ---------+---------+---------+---------+---------+---------+ 1020
                TAGTAAGGATGCAGTGTAGGCATTCGACCCTGTCTCGGGTCTCCCACTCCTCCGGAGGTC
                 S  F  L  R  H  I  R  K  L  G  Q  S  P  E  G  E  E  A  S  R

                GCAGGGTATGACCCGTCACAGCCACCCAGGCCTTGGGACTAGCCAGTCTCCCAAGTGGTG
1021            ---------+---------+---------+---------+---------+---------+ 1080
                CGTCCCATACTGGGCAGTGTCGGTGGGTCCGGAACCCTGATCGGTCAGAGGGTTCACCAC
                 Q  G  M  T  R  H  S  H  P  G  L  G  T  S  Q  S  P  K  W  V
```

FIG. 6B

```
                ACAACCAGGTGGATGCCAAGGAAGGCCAAGTGGACTGACTCCTAGCTTTTCTTTCCTCCA
1081            ---------+---------+---------+---------+---------+---------+ 1140
                TGTTGGTCCACCTACGGTTCCTTCCGGTTCACCTGACTGAGGATCGAAAAGAAAGGAGGT
                T  T  R  W  M  P  R  K  A  K  W  T  D  S

                GCCCTTTTGATCTCCTTCCCTGATCCTTGTCCCCCCGGACTGGCCTCTGTTGGAAAGTCCA
1141            ---------+---------+---------+---------+---------+---------+ 1200
                CGGGAAAACTAGAGGAAGGGACTAGGAACAGGGGGCCTGACCGGAGACAACCTTTCAGGT

                AGACCGTGGGTGTGATGCATGGCACTGGGGTATGGGGCTTCCCAAGTATGTCCCCAGCCT
1201            ---------+---------+---------+---------+---------+---------+ 1260
                TCTGGCACCCACACTACGTACCGTGACCCCATACCCCGAAGGGTTCATACAGGGGTCGGA

                CTGTCCTTTGTTGCTGCCACCCTCTATGGAAACTGAGGAGGTATTCAAAAATGGATTTGG
1261            ---------+---------+---------+---------+---------+---------+ 1320
                GACAGGAAACAACGACGGTGGGAGATACCTTTGACTCCTCCATAAGTTTTTACCTAAACC

                GGGCCATCCTTCCTGCACCTTGCACGCACATATGCATTGCGTGGCTGTTCTGTGCTTTGC
1321            ---------+---------+---------+---------+---------+---------+ 1380
                CCCGGTAGGAAGGACGTGGAACGTGCGTGTATACGTAACGCACCGACAAGACACGAAACG

                TGACTGTGGGTGGTCCTGCTTGTGTTGTAGCCCTTTAGTTCCTCCTCTTTCCAACCAATA
1381            ---------+---------+---------+---------+---------+---------+ 1440
                ACTGACACCCACCAGGACGAACACAACATCGGGAAATCAAGGAGGAGAAAGGTTGGTTAT

                AAGACAAACAGAACAATG
1441            ---------+--------- 1458
                TTCTGTTTGTCTTGTTAC
```

FIG. 6C

FIG. 7A

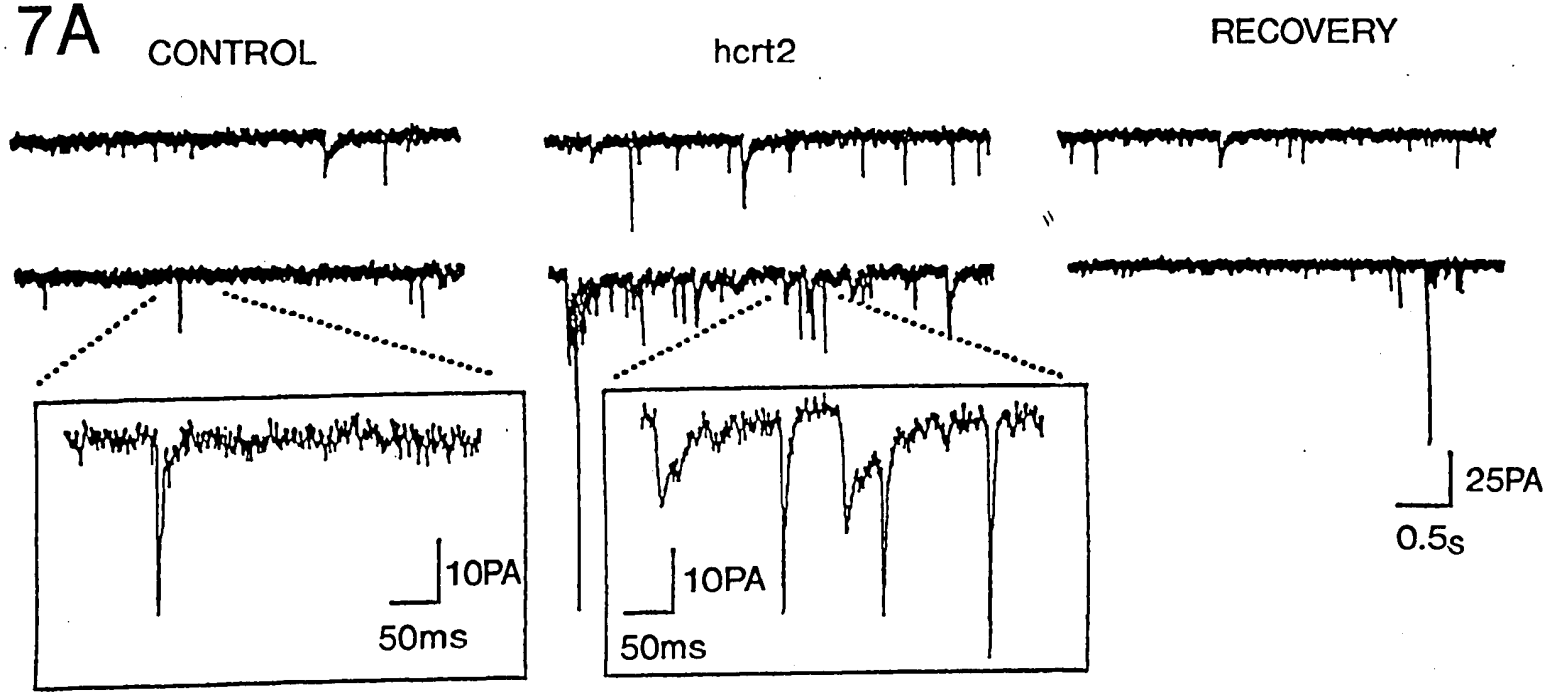


FIG. 7B